

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 42.1298 Seconds

(without alignments)
1349.183 Million cell updates/sec

Title: US-09-939-537-37

Perfect score: 591

Sequence: 1 TRFSSASBPAYQQGNQLY.....LSTATQTYDALMQALPPR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	572	96.8	163	1	CD3Z_PIG	Q9XJ99 sus scrofa
2	561.5	95.0	164	1	CD3Z_HUMAN	P20968 homo sapien
3	496	83.9	165	1	CD3Z_RABIT	O91uf8 oryctolagus
4	476.5	80.6	164	1	CD3Z_MOUSE	P24161 mus musculus
5	471.5	79.8	166	1	CD3Z_SHEEP	P29329 ovie aries
6	378.5	64.0	206	1	CD3H_MOUSE	P29020 mus musculus
7	303	51.3	322	2	Q6KAV0	O6kav0 homo sapien
8	90.5	15.3	612	2	Q7SYB5	O7syb5 brachydanio
9	90.5	15.3	628	2	Q6TNH8	O6tnh8 brachydanio
10	86	14.6	1167	1	WCI1_NEUCR	O01371 neurospora
11	86	14.6	1262	2	Q7RYA7	O7rya7 neurospora
12	85	14.4	172	2	Q8CMD5	O8cmd5 streptococc
13	81.5	13.8	744	2	Q754G7	O754g7 ashbya gosw
14	81	13.7	1133	2	Q7XK73	O7xk73 oryza sativ
15	80	13.5	692	2	Q19579	O19579 caenorhabdi
16	79.5	13.5	868	2	Q9VYF5	O9vly5 drosophila
17	78.5	13.3	312	2	Q6SLR3	O6slr3 bacillus th
18	78.5	13.3	501	2	Q6UUE1	O6ueu1 oryza sativ
19	78	13.2	919	2	Q9LPD8	O9lpd8 arabidopsis
20	78	13.2	937	2	Q9MAL4	O9mal4 arabidopsis
21	77.5	13.1	328	2	Q6RGA4	O6rga4 rhodococcus
22	77	13.0	889	2	Q6H4V8	O6h4v8 oryza sativ
23	77	13.0	928	2	Q6H4V9	O6h4v9 oryza sativ
24	76.5	12.9	521	1	DB45_DROME	O07806 drosophila
25	75.5	12.8	169	2	Q8RF77	O8rf77 fusobacteri
26	75.5	12.8	169	2	Q8RG33	O8rg33 fusobacteri
27	75.5	12.8	169	2	Q8RHV6	O8rhv6 fusobacteri
28	75.5	12.8	924	2	Q92QJ4	O92qj4 rhizobium m
29	75	12.7	171	2	Q9KK22	O9kk22 streptococc
30	75	12.7	354	2	Q91E80	O91e80 cydia pomon
31	74.5	12.6	596	2	Q6PA69	O6pa69 xenopus lae

32	74.5	12.6	761	2	Q7MNX6	Q7mnx6 vibrio vuln
33	74.5	12.6	761	2	Q8DEI4	Q8dei4 vibrio vuln
34	74	12.5	136	2	Q39681	Q39681 daucus caro
35	74	12.5	364	2	Q6C3D3	Q6c3d3 yarrowia li
36	74	12.5	450	2	Q8VE87	Q8ve87 mus musculu
37	74	12.5	748	2	Q95TP4	Q95tp4 drosophila
38	74	12.5	820	2	Q8CD02	Q8cd02 mus musculu
39	74	12.5	867	2	Q8IKI7	Q8iki7 plasmodium
40	74	12.5	1330	2	Q8K4P0	Q8k4p0 mus musculu
41	74	12.5	3190	2	Q01368	Q01368 drosophila
42	74	12.5	3276	2	Q9WJ21	Q9wj21 drosophila
43	73.5	12.4	122	1	GS1B_BACSU	P26907 bacillus su
44	73.5	12.4	360	1	RLPA_YERPE	Q8zdg6 yersinia pe
45	73.5	12.4	360	2	Q6BDF1	Q6bdf1 yersinia pe

ALIGNMENTS

RESULT 1	CD3Z_PIG	STANDARD,	PRT,	163 AA.
AC	Q9XSJ9;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor T3 zeta chain).			
GN	Name=CD3Z;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.			
OX	NCBI_TaxId=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Minesota miniature swine;			
RA	Jie H.-B., Yim D., Kim Y.B.;			
RT	"The molecular cloning of porcine CD3 zeta.";			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: Probable role in assembly and expression of the TCR complex as well as signal transduction upon antigen triggering.			
CC	- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the cell surface with the invariant subunits of CD3 labeled gamma.			
CC	delta, epsilon, zeta, and eta (By similarity).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- PTM: Phosphorylated on Tyr residues after T-cell receptor triggering (By similarity).			
CC	- SIMILARITY: Belongs to the CD3Z/FCER1G family.			
CC	- SIMILARITY: Contains 3 ITAM domains.			
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CC	-----			
DR	EMBL; AF153630; AAD34640.1; -			
DR	InterPro; IPR003110; ITAM.			
DR	Pfam; PF02189; ITAM; 3.			
DR	SMART; SM00077; ITAM; 3.			
KW	Phosphorylation; Receptor; Repeat; Signal; T-cell; Transmembrane.			
FT	CHAIN	1	21	
FT	STGNL	22	163	
FT	FT			
FT	DOMAIN	22	30	
FT	TRANSMEM	31	51	
FT	DOMAIN	52	163	
FT	DOMAIN	69	89	
FT	DOMAIN	107	128	
FT	DOMAIN	138	158	
FT	DOMAIN			
FT	ITAM 1.			
FT	Cytoplasmic (Potential).			
FT	ITAM 2.			
FT	ITAM 3.			

FT DISUFID 32 32 Interchain (Potential).
QT MOD RES 152 152 Phosphotyrosine (By similarity).
SQ SEQUENCE 163 AA; 18566 MW; 34898620B67167C7 CRC64;
Query Match 96.8%; Score 572; DB 1; Length 163;
Best Local Similarity 97.3%; Pred. No. 1.2e-46;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 RFSRSAPPAVYOGQGNLYNELNGRREYDVLDKRGKRPENMGKPRKRNQEGLYNEL 61
DB 54 KFRSRADAPAYOGQGNLYNELNGRREYDVLDKRGKRPENMGKPRKRNQEGLYNEL 113
QY 62 QKDKMAVAVSEIGMKERRRGKHGDLGYQGLSTATQDYDALHMOALPPR 111
DB 114 QKDKMAVAVSEIGMKERRRGKHGDLGYQGLSTATQDYDALHMOALPPR 163
RESULT 2
CD32_HUMAN STANDARD; PRT; 164 AA.
ID CD32_HUMAN
AC P20963; O8TX4;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor
DE 13 zeta chain).
GN Name=CD32; Synonyms=132, TCR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
NP SEQUENCE FROM N.A.
RX MEDLINE=89071765; PubMed=2974162;
RA Weisman A.M., Hou D., Orloff D.G., Modi W.S., Senanez H.,
RA O'Brien S.J., Klausner R.D.;
RT "Molecular cloning and chromosomal localization of the human T-cell
RT receptor zeta chain: distinction from the molecular CD3 complex";
RT Proc. Natl. Acad. Sci. U.S.A. 85:9709-9713 (1988).
[2]
NP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Cassavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Kodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
NP INTERACTION WITH HIV-1 NEF.
RX PubMed=10224289;
RA Xu X.-N., Lafert B., Sreaton G.R., Kraft M., Wolf D., Kolanus W.,
RA Wongkolapap Y., McMichael A.J., Baur A.S.;
RT "Induction of Fas ligand expression by HIV involves the interaction of
RT Nef with the T cell receptor zeta chain";
RT J. Exp. Med. 189:1489-1496 (1999).
[4]
NP INTERACTION WITH SLA.

RX MEDLINE=99380595; PubMed=10449770; DOI=10.1073/pnas.96.17.9775;
RA Tang J., Sawadhihosol S., Chang J.-H., Burkoff S.J.;
RT "SLAP, a dimeric adapter protein, plays a functional role in T cell
RT receptor signaling";
RT Proc. Natl. Acad. Sci. U.S.A. 96:9775-9780 (1999).
RN [5]
RP INTERACTION WITH DOCK2.
RX MEDLINE=22165501; PubMed=12176041; DOI=10.1016/S0006-291X(02)00931-2;
RA Nishihara H., Maeda M., Tsuda M., Makino Y., Sawa H., Nagashima K.,
RA Tanaka S.;
RT "DOCK2 mediates T cell receptor-induced activation of Rac2 and IL-2
RT transcription";
RT Biochem. Biophys. Res. Commun. 296:716-720 (2002).
RN [6]
RP PHOSPHORYLATION SITES TYR-83; TYR-111; TYR-123 AND TYR-142.
RX PubMed=12522270; DOI=10.1073/pnas.2436191100;
RA Salomon A.R., Ficarro S.B., Brill L.W., Brinker A., Phung Q.T.,
RA Ericson C., Sauer K., Brock A., Horn D.M., Schultz P.G., Peters E.C.;
RT "Profiling of tyrosine phosphorylation pathways in human cells using
RT mass spectrometry";
RT Proc. Natl. Acad. Sci. U.S.A. 100:443-448 (2003).
RN [7]
RP STRUCTURE BY NMR OF 136-149.
RX MEDLINE=93201600; PubMed=7680960; DOI=10.1016/0092-8674(93)90405-F;
RA Wakeman G., Shoelson S.E., Pant N., Cowburn D., Kurlyan J.;
RT "Binding of a high affinity phosphotyrosyl peptide to the Src SH2
RT domain: crystal structures of the complexed and peptide-free forms";
RT Cell 72:779-790 (1993).
RL CC
CC -1- FUNCTION: Probable role in assembly and expression of the TCR
CC complex as well as signal transduction upon antigen triggering.
CC -1- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a
CC TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the
CC cell surface with the invariant subunits of CD3 labeled gamma,
CC delta, epsilon, zeta, and eta. CD3-zeta forms either homodimers or
CC heterodimers with CD3-eta. Interacts with SLA and SLA2. Interacts
CC with DOCK2. Interacts with HIV-1 Nef protein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=CD-3-zeta;
CC IsoId=P20963-1; Sequence=Displayed;
CC Name=CD-3-eta;
CC IsoId=P20963-2; Sequence=Not described;
CC -1- PTM: Phosphorylated on Tyr residues after T-cell receptor
CC triggering (By similarity).
CC -1- SIMILARITY: Belongs to the CD32/PCERIG family.
CC -1- SIMILARITY: Contains 3 ITAM domains.
CC
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CC
CC EMBL: J04132; AAA60394.1; -
CC EMBL: BC025703; AAH25703.1; -
CC PIR: A31768; A31768.136-149.
CC PDB: 1TCE; NMR; B=136-149.
CC Genew; HGNC:1677; CD32.
CC H-InvDB; HIX0001296; -
CC MIM: 186780; -
CC GO: GO:0005886; C:Plasma membrane; TAS.
CC GO: GO:0042101; C:T-cell receptor complex; TAS.
CC GO: GO:0005515; F:protein binding; IPI.
CC GO: GO:0042803; F:protein homodimerization activity; NAS.
CC InterPro; IPR003110; ITAM.
CC Pfam; PF02189; ITAM; 3.
CC SMART; SM00077; ITAM; 3.
CC 3D-structure; Alternative splicing; Phosphorylation; Receptor; Repeat;
CC Signal; T-cell; Transmembrane.
CC SIGNAL 1
CC 21

```

FT CHAIN 22 164 T-cell surface glycoprotein CD3 zeta
FT DOMAIN 22 30 chain.
FT TRANSMEM 31 51 Extracellular (Potential).
FT DOMAIN 52 164 Potential.
FT DOMAIN 69 89 Cytoplasmic (Potential).
FT DOMAIN 108 129 ITAM 1.
FT DOMAIN 139 159 ITAM 2.
FT DISULFID 32 32 Interchain (Potential).
FT MOD_RES 83 83 Phosphotyrosine.
FT MOD_RES 111 111 Phosphotyrosine.
FT MOD_RES 123 123 Phosphotyrosine.
FT MOD_RES 142 142 Phosphotyrosine.
FT MOD_RES 153 153 Phosphotyrosine.
FT CONFLICT 60 61 DA -> EP (in Ref. 1).
FT CONFLICT 101 101 Missing (in Ref. 1).
SQ SEQUENCE 164 AA; 18696 MW; 9408260374856B9 CRC64;

Query Match 95.0%; Score 561.5; DB 1; Length 164;
Best Local Similarity 96.4%; Pred. No. 1.2e-45;
Matches 107; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 RRSRSAPPAAYQGQGNQLYNELNGRREBYDVLDRGRDPEWGGKPR-RKKNPQEGLYNE 60
DB 54 KFSRSADAPAYQGQGNQLYNELNGRREBYDVLDRGRDPEWGGKPRKKNPQEGLYNE 113
QY 61 LQDKMAEAYSEIGMKGERRGKHGDLGYGLSTATKDTYDALHMQALPPR 111
DB 114 LQDKMAEAYSEIGMKGERRGKHGDLGYGLSTATKDTYDALHMQALPPR 164

RESULT 3
CD3Z_RABIT STANDARD; PRT; 165 AA.
ID CD3Z_RABIT
AC Q9TUF8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor
T3 zeta chain).
GN Name=CD3z;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J x Chdb.HM;
RA Isono T., Nishimura M.;
RT "Rabbit CD3 zeta."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probable role in assembly and expression of the TCR
CC complex as well as signal transduction upon antigen triggering.
CC -1- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a
CC TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the
CC cell surface with the invariant subunits of CD3 labeled gamma,
CC delta, epsilon, zeta, and eta (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Phosphorylated on Tyr residues alter T-cell receptor
CC triggering (By similarity).
CC -1- SIMILARITY: Belongs to the CD3z/FCER1G family.
CC -1- SIMILARITY: Contains 3 ITAM domains.
CC -----
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CC -----
CC EMBL; AB035152; BAA86994.1; -.
CC InterPro; IPR003110; ITAM.

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DR Pfam; PF02189; ITAM; 3.
DR SMART; SM00077; ITAM; 3.
KW Phosphorylation; Receptor; Repeat; Signal; T-cell; Transmembrane.
FT SIGNAL 1 21 By similarity. T-cell; Transmembrane.
FT CHAIN 22 165 T-cell surface glycoprotein CD3 zeta
FT DOMAIN 22 30 chain.
FT TRANSMEM 31 51 Extracellular (Potential).
FT DOMAIN 52 165 Potential.
FT DOMAIN 69 89 Cytoplasmic (Potential).
FT DOMAIN 107 128 ITAM 1.
FT DOMAIN 140 160 ITAM 2.
FT DISULFID 32 32 Interchain (Potential).
FT MOD_RES 154 154 Phosphotyrosine (By similarity).
SQ SEQUENCE 165 AA; 18773 MW; 3183136130BAAAF5 CRC64;

Query Match 83.9%; Score 496; DB 1; Length 165;
Best Local Similarity 84.8%; Pred. No. 2.2e-39;
Matches 95; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 2 RRSRSAPPAAYQGQGNQLYNELNGRREBYDVLDRGRDPEWGGKPRKKNPQEGLYNE 61
DB 54 KFSRGEDEVSPQGHQTQLYNELNGRREBYDVLDRGRDPEWGGKPRKKNPQEGLYNE 113
QY 62 QDKMAEAYSEIGMKGE--RRRGKHGDLGYGLSTATKDTYDALHMQALPPR 111
DB 114 QDKMAEAYSEIGMKGE--RRRGKHGDLGYGLSTATKDTYDALHMQALPPR 165

RESULT 4
CD3Z_MOUSE STANDARD; PRT; 164 AA.
ID CD3Z_MOUSE
AC P24161; O9D3G3;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor
T3 zeta chain).
GN Name=CD3z; Synonyms=Tcrz;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC MEDLINE=88145643; PubMed=3278377;
RA Weissman A.M., Banlyash M., Hou D., Samelson L.E., Burgess W.H.,
RA Klausner R.D.;
RT "Molecular cloning of the zeta chain of the T cell antigen receptor."
RL Science 239:1018-1021 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Banlyash M., Heu V.W., Seldin M.F., Klausner R.D.;
RT "The isolation and characterization of the murine T cell antigen
RT receptor zeta chain gene."
RL J. Biol. Chem. 264:13252-13257 (1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Mikado I., Oseto N., Saito K., Suzuki H., Yamataka H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T.,
RA Baldirelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirmel L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochiaia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaesteland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmerand T., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

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RA Nagoshi D.R., Matsuda L., Matchinomi L., Mckenzie Z., Nishizawa T., Nishizawa G.,
RA Nagoshi T., Numata K., Okido T., Pavan W.J., Pertea G., Peele G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ranaachandran S.,
RA Ravasi T., Reed J.C., Reed D.T., Reid U., Ring B.Z., Ringswald M.,
RA Sandelin A., Schneider C., Seiple C.A., Setou M., Shimada K.,
RA Saito A., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Velazquez R., Wagner L., Wahlstedt C., Wang Y., Wetanabe Y., Wells C.,
RA Vitarito R., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carinici P., Hayatsu N.,
RA Hirozane-Kikukawa T., Komori H., Nakamura M., Sakazume N., Sato K.,
RA Shihara T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocari K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaunashiki A., Yoshino W., Westerton R., Lander E.S., Rogers J.,
RA Birney E., Hayashiaki Y.,
RT [Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."]
RL Nature 420:563-573(2002).

[4]
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE=Hematopoietic;
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Straubeberg R.L., Petrosold E.A., Grioux L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Butler N.K.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Scheffer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Schetz T.E.,
RA Staphenonko M., Soares M.B., Bonaldi M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Mozy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodigesley A.C., Grimwood J., Schmutter J., Myers R.M.,
RA Butterfield V.S.N., Krzyminski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schin J.E., Jones S.J.M., Merritt M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN PARTIAL SEQUENCE.
RP MEDLINE=90239005; PubMed=2139725;
RX Jin Y.J., Clayton L.K., Howard F.D., Koyasu S., Sieh W.,
RA Steinbüchel R., Tarr G.B., Reinherz E.L.,
RT "Molecular cloning of the CD3 eta subunit identifies a CD3 zeta-
RT related product in thymus-derived cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3319-3323(1990).
RN [6]
RN ALTERNATIVE SPLICING.
RP PubMed=21505967.
RX Ohno H., Saito T.,
RT "CD3 zeta and eta chains are produced by alternative splicing from a
RT common Gene.";
RL Int. Immunol. 2:1117-1119(1990).
RN [7]
RP ERRATUM.
RA Ohno H., Saito T.,
RL Int. Immunol. 4:1339-1339(1992).
RN [8]
RN INTERACTION WITH SLA.
RX MEDLINE=20130290; PubMed=10662792;
RA Soehnleweki T., Pandey A., Dixit V.M., Weiss A.,
RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell
RT receptor signaling.";
RL J. Exp. Med. 191:463-474(2000).
RN [9]
RN INTERACTION WITH SLA2.
RP MEDLINE=22013997; PubMed=11891219; DOI=10.1074/jbc.M110318200;
RX Pandey A., Ibarrola N., Kratchmarova I., Fernandez M.M.,
RN Constantinescu S.N., Ohara O., Sawasdi Kosol S., Lodish H.F., Mann M.,

Query Match	Best Local Similarity	Matches	Score	DB 1	Length
QY	80.6%;	83.8%;	5;	Mismatches 12;	Indels 1;
Db	2	RFSHSAEPYAGCGNQLVNEMLGRRREYDVLDKRRGRDPMGK-PRKKPOEGLYNE	60		
QY	54	KFSRSATFANLDDPOLVNEMLIGRREEDVLEKRRADPMGKQRRRNPQBSVNYA	113		
Db	61	LQDKMAEAVSEIGMKGRPRGKHGLVQGLSTATKDTYDALHMQALPPR	111		
QY	114	LQDKMAEAVSEIGTKGRGRGKHGLVQGLSTATKDTYDALHMQTLAPR	164		

RESULT 5

CD3Z_SHEEP

ID CD3Z_SHEEP

AC P293291

STANDARD;

PRT;

166 AA.

```

DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor
DE T3 zeta chain).
GN Name=CD3z; (Sheep).
OS Ovis aries (Sheep).
OC Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxId=9940;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=White alpine;
RX MEDLINE=9311305; PubMed=8420837;
RA Hein W.R., Tunncliffe A.;
RT "Invariant components of the sheep T-cell antigen receptor: cloning of
RT the CD3 epsilon and zeta chains."
RL Immunogenetics 37:279-284(1993).
CC -1- FUNCTION: Probable role in assembly and expression of the TCR
CC complex as well as signal transduction upon antigen triggering.
CC -1- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a
CC TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the
CC cell surface with the invariant subunits of CD3 labeled gamma,
CC delta, epsilon, zeta, and eta.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Phosphorylated on Tyr residues after T-cell receptor
CC triggering (By similarity).
CC -1- SIMILARITY: Belongs to the CD3z/FCER1G family.
CC -1- SIMILARITY: Contains 3 ITAM domains.
CC -----
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CC -----
DR EMBL; Z12968; CA78312.1; -
DR PIR; I46424; I46424.
DR InterPro; IPR003110; ITAM.
DR Pfam; PF02189; ITAM; 3.
DR SMART; SM00077; ITAM; 3.
KM Phosphorylation; Receptor; Repeat; Signal; T-cell; Transmembrane.
FT CHAIN 1 21 By similarity.
FT CHAIN 2 166 T-cell surface glycoprotein CD3 zeta
FT CHAIN 3 166 chain.
FT DOMAIN 22 30 Extracellular (Potential).
FT TRANSMEM 31 51 Potential.
FT DOMAIN 52 166 Cytoplasmic (Potential).
FT DOMAIN 69 89 ITAM 1.
FT DOMAIN 108 129 ITAM 2.
FT DOMAIN 141 161 ITAM 3.
FT DISULFID 32 32 Interchain (Potential).
FT MOD RES 155 155 Interphosphorylation (By similarity).
SQ SEQUENCE 166 AA; 18704 MW; E7D89AD84E58311A CRC64;

```

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ID CD3H_MOUSE STANDARD; PRT; 206 AA.
AC P29020;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T-cell surface glycoprotein CD3 eta chain precursor (T-cell receptor
DE T3 eta chain).
GN Name=CD3z; Synonyms=CD3h;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC MEDLINE=90239005; PubMed=2139725;
RX Jin Y.J., Clayton L.K., Howard F.D., Koyasu S., Sieh M.,
RA Clayton L.K., D'Adamo L., Sieh M., Husey R.E., Koyasu S.,
RA Reinherz E.L., Howard F.B.;
RT "CD3 eta and CD3 zeta are alternatively spliced products of a common
RT genetic locus and are transcriptionally and/or post-transcriptionally
RT regulated during T-cell development."
RL Proc. Natl. Acad. Sci. U.S.A. 87:3319-3323(1990).
RN (2)
RP SEQUENCE OF 144-206 FROM N.A.
RX MEDLINE=91271358; PubMed=1828894;
RA Clayton L.K., D'Adamo L., Sieh M., Husey R.E., Koyasu S.,
RA Reinherz E.L., Howard F.B.;
RT "CD3 eta and CD3 zeta are alternatively spliced products of a common
RT genetic locus and are transcriptionally and/or post-transcriptionally
RT regulated during T-cell development."
RL Proc. Natl. Acad. Sci. U.S.A. 88:5202-5206(1991).
RN (3)
RP SEQUENCE OF 144-206 FROM N.A.
RX PubMed=2150596;
RA Ohno H., Saito T.;
RT "CD3 zeta and eta chains are produced by alternative splicing from a
RT common gene."
RL Int. Immunol. 2:1117-1119(1990).
RN (4)
RP ERRATUM.
RA Ohno H., Saito T.;
RL Int. Immunol. 4:1339-1339(1992).
CC -1- FUNCTION: Probable role in assembly and expression of the TCR
CC complex as well as signal transduction upon antigen triggering.
CC -1- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a
CC TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the
CC cell surface with the invariant subunits of CD3 labeled gamma,
CC delta, epsilon, zeta, and eta. CD3-eta can be complexed in a
CC heterodimeric form with CD3-zeta subunit. CD3-eta homodimer has
CC not been observed.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=CD-3-eta;
CC IsoId=P29020-1; Sequence=Displayed;
CC Name=CD-3-zeta;
CC IsoId=P24161-1; Sequence=External;
CC -1- SIMILARITY: Belongs to the CD3z/FCER1G family.
CC -1- SIMILARITY: Contains 3 ITAM domains.
CC -----
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CC -----
DR EMBL; M33158; AAA37398.1; -
DR EMBL; M76711; AAA40403.1; -
DR PIR; A35900; A35900.
DR MGI; 88334; CD3z.
DR InterPro; IPR003110; ITAM.
DR Pfam; PF02189; ITAM; 2.
DR SMART; SM00077; ITAM; 2.

```

```

KW Alternative splicing; Direct protein sequencing; Receptor; Repeat;
KM Signal; T-cell; Transmembrane.
FT CHAIN 1 21
FT 22 206 T-cell surface glycoprotein CD3 eta
FT DOMAIN 22 30 chain.
FT TRANSMEM 31 51 Extracellular (Potential).
FT DOMAIN 52 206 Potential.
FT DOMAIN 69 89 Cytoplasmic (Potential).
FT DOMAIN 108 129 ITAM 1.
FT DOMAIN 139 159 ITAM 2.
FT DISULFID 32 32 ITAM 3.
SQ SEQUENCE 206 AA; 23339 MW; 829256A2CF4E444 CRC64;

Query Match 64.0%; Score 378.5; DB 1; Length 206;
Best Local Similarity 82.2%; Pred. No. 4.3e-28;
Matches 74; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 2 RFSRSAPPPAYOQGNQLYNELNGRREYDVLDRGRGDPENGGK-PRKKNPQEGLYNE 60
Db 54 KFSRSAPETANIQDPNQLYNELNGRREYDVEKRRARDPENGGKQRRRNPEGVYNA 113
QY 61 LQDKMAEYSEIGMKGERRGKGDGLYQ 90
Db 114 LQDKMAEYSEIGTKGERRRGKGDGLYQ 143

RESULT 7
Q6KAVO PRELIMINARY; PRT; 322 AA.
AC Q6KAVO;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ46519.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Niinomiya K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hiro Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK128376; BAC87407.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IEA.
DR InterPro; IPR003110; ITAM.
DR Pfam; PF02189; ITAM; 1.
DR SMART; SM00077; ITM; 1.
SQ SEQUENCE 322 AA; 34926 MW; D4461DBEC26BC011 CRC64;

Query Match 51.3%; Score 303; DB 2; Length 322;
Best Local Similarity 60.5%; Pred. No. 1.1e-20;
Matches 69; Conservative 9; Mismatches 12; Indels 24; Gaps 6;

QY 2 RFSRSAPPPAYOQGNQLYNELNGRREYDVLDRGRGDPENGGK-PRKKNPQEGLYNE 60
Db 54 KFSRSADAPPYQGGNQLYNELNGRREYDVLDRGRGDPENGGKPKRRKNPQEGLYNV 113
QY 61 LQDK-----KMAEYSEIGMKGE-----RRRG-KG-----HDGLYQGL 92
Db 114 SRDLTFDGLGKLEGLLE-GRSGAGAGAGGGLQKRGKRGWRAPAEGLLEGL 166

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RESULT 8
Q7SYB5 PRELIMINARY; PRT; 612 AA.
AC Q7SYB5;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Similar to differentially expressed in FDCP 6.
GN ORFNames=zgc:63721;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shchepochko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; BC054935; AAH54935.1; -.
DR HSSP; O08967; 1FGV.
DR ZFIN; ZDB-GENE-040426-1246; zgc:63721.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_1like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR01036; PH-related.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
SQ SEQUENCE 612 AA; 72090 MW; 778DBDC5FEBB689 CRC64;

Query Match 15.3%; Score 90.5; DB 2; Length 612;
Best Local Similarity 28.3%; Pred. No. 4.2;
Matches 28; Conservative 25; Mismatches 43; Indels 3; Gaps 3;

QY 12 YQGGNQLYNELNGRREYDVLDRR-GRDPMGGKPRKKNPQEGLYNELQDKMAEY 70
Db 309 YVGGKSLHKDKLTKRRDRQRRKRRKKEBELQRLRLQRRERKMAELILKKAQNG 368
QY 71 SEIGM-KGERRRGKGDGLYQGLSTATYKDTYDA-LHMQA 107
Db 369 AQAMLEQDEQRRRQGHQHLQALRIQLKEAFBARASMQA 407

RESULT 9
Q6TNUB

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```
ID 06TNU8 PRELIMINARY; PRT; 628 AA.
AC 06TNU8;
DT 05-JUL-2004 (TRENBLREL. 27, Last Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Differentially expressed in FDCP 6-like protein.
GN Name=DF6; ORFNames=zgc:63721;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.,
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AY391419; AAQ91231.1; -.
DR ZFIN; ZDB-GENE-040426-1246; zgc:63721.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_1like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH-related.
DR Pfam; PF00169; PH.1.
DR SMART; SM00233; PH.1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR SEQUENCE 628 AA; 74478 MW; CF69DCA28BA944F0 CRC64;

Query Match 15.3%; Score 90.5; DB 2; Length 628;
Best Local Similarity 28.3%; Pred. No. 4.3;
Matches 28; Conservative 23; Mismatches 43; Indels 3; Gaps 3;

Qy 12 YQGGQNLVNLIGRREBYDVLKRR-GRDPEGKPRRRKQEGLYNELQDKMAEAY 70
Db 309 YVGGKSLHMDLTKRRDRQREGRKEAKEQELQRLALQGBRRERMALEILKEAQ 368
Db 369 AQAMLEQDEQRHROHQHQLHQLLEIQLEAEARASQA 407

RESULT 10
WCI_NEUCR STANDARD; PRT; 1167 AA.
ID WCI_NEUCR
AC 001371;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE White collar 1 protein (WCI1).
GN Name=WCI-1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=74-OR23-1A / FGSC 987;
RA MEDLINE=96203083; PubMed=8612589;
RA Ballario P., Valtorioso P., Magrelli A., Talora C., Cabibbo A.,
RA Macino G.,
RA "White collar-1, a central regulator of blue light responses in
RA Neurospora, is a zinc finger protein.",
RA EMBO J. 15:1650-1657(1996).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Ballario P.,
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as a transcription factor involved in light
CC regulation. Binds and affects blue light regulation of the AL-3
CC gene. WCI1 and WCI2 proteins interact via homologous PAS domains,
```

```
CC bind to promoters of light regulated genes such as FRQ, and
CC activate transcription.
CC -1- SUBUNIT: Heterodimer of WCI1 and WCI2 (potential).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- INDUCTION: By blue light.
CC -1- DOMAIN: The glutamine-rich domain might function in activating
CC gene expression.
CC -1- SIMILARITY: Contains 1 GATA-type zinc finger.
CC -1- SIMILARITY: Contains 3 PAS (PER-ARNT-SIM) dimerization domains.
CC -1- SIMILARITY: Contains 2 PAS-associated C-terminal (PAC) domains.
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CC EMBL; X94300; CAA63964.2; -.
DR HSSP; P1679; 1GNF.
DR TRANSFAC; T02819; -.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR000679; ZnF_GATA.
DR Pfam; PF00320; GATA.1.
DR Pfam; PF00785; PAC.1.
DR Pfam; PF00989; PAS.2.
DR SMART; SM00086; PAC; 2.
DR SMART; SM00091; PAS; 3.
DR SMART; SM00401; ZnF_GATA.1.
DR TIGRFAMs; TIGR00229; sensory box; 3.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
DR PROSITE; PS01114; GATA_ZN_FINGER_2; 1.
DR PROSITE; PS01112; PAS; 3.
DR KX Activator; DNA-binding; Nuclear protein; Repeat;
DR Transcription regulation; zinc-finger.
FT DOMAIN 16 61 PAS 1.
FT DOMAIN 469 508 PAC 1.
FT DOMAIN 574 644 PAS 2.
FT DOMAIN 650 691 PAC 2.
FT DOMAIN 693 763 PAS 3.
FT ZN_FING 934 959 GATA-type.
FT DOMAIN 21 57 Poly-Gln.
FT DOMAIN 329 333 Poly-Pro.
SQ SEQUENCE 1167 AA; 127454 MW; 6489D04DAB50EB38 CRC64;

Query Match 14.6%; Score 86; DB 1; Length 1167;
Best Local Similarity 24.8%; Pred. No. 24;
Matches 33; Conservative 19; Mismatches 49; Indels 32; Gaps 6;

Qy 9 PPAYQGGQNLV-----NELNLIGRREBYDVLKRRGRDPEMGKPRR-----KN 52
Db 71 PPTTNGQNSTIHASDVMTSGSDSLDIQLQNLDEHRRRSVPQYGGQRRRLSMFDYAN 130
Qy 53 PGGLYNELQDKMAEAYSB-----LKGERRRKGK-----HGQLQGLS---TATK 97
Db 131 PNDG-FSDYQLDMSGNYGDMTGGMGSHSPYAGQNIAMSDHSGYSHMSPNYGMN 189
Qy 98 DTYDALHMQALPP 110
Db 190 MTPYNIIMTHSP 202

RESULT 11
Q7RVA7 PRELIMINARY; PRT; 1262 AA.
ID Q7RVA7
AC Q7RVA7;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE White collar 1 protein (WCI1).
```



```

GN Name=NCU02356.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCB1_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R.W., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seltzer K.O., Kinney J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierke S.,
RA Kamal M., Kamysseil M., Mauceli E., Bieleke C., Rudd S., Fishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cognoli C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0 (2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX0100358; EAA30541.1; -.
CC HSSP; P17679; 1GNF.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR000679; znf_GATA.
DR Pfam; PF00320; GATA; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR TIGRPFAMS; TIGR00229; sensory_box; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
DR PROSITE; PS00114; GATA_ZN_FINGER_2; 1.
DR PROSITE; PS00112; PAS; 3.
DR PROSITE; PS00112; PAS; 3.
SQ SEQUENCE 1262 AA; 138115 MW; F39E72B09DE1E5F1 CRC64;

Query Match 14.8%; Score 86; DB 2; Length 1262;
Best Local Similarity 24.8%; Pred. No. 26;
Matches 33; Conservative 19; Mismatches 49; Indels 32; Gaps 6;

QY 9 PPAVQGGONOLY-----NELNIGRREYVDLKKRRGRDPENWGKRRR-----KN 52
DB 71 PPTNQGNSTIHASDVMTSGSDSLDEIIQNLDEMRHRSVPQYGGQTRRLSMFDYAN 130
QY 53 PDELVNELOKDKMAEAYSE-----IGKKGRRRGKG-----HDGLYGOOLS---TATK 97
DB 131 PNEG-FSDYQLDNNSGNYGDMTGMGSHSSPYAGONTAMSDHSGYSHMSFNWGMN 189
QY 98 DTYDALHMOALPP 110
DB 190 MTYPNLMNHYSP 202

RESULT 12
Q8CMD5 PRELIMINARY; PRT; 172 AA.
AC O8CMD5;
DT 01-MAR-2003 (TRENDELrel. 23, Created)
DT 01-MAR-2003 (TRENDELrel. 23, Last sequence update)
DT 25-OCT-2004 (TRENDELrel. 28, Last annotation update)
DE Hypothetical protein SMU.566c (Hypothetical protein SMU.1379)

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DE (Hypothetical protein SMU.1408c) (Hypothetical protein
DE SMU.1894c).
GN OrderedLocName=SMU.1379, SMU.1408c, SMU.1894c, SMU.766;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U0A159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; Pubmed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans U0A159, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
RL EMBL; AE014901; AAN58307.1; -.
DR EMBL; AE014918; AAN58486.1; -.
DR EMBL; AE014971; AAN59047.1; -.
DR EMBL; AE014974; AAN59073.1; -.
DR EMBL; AE015015; AAN59507.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR002514; Transposase_8.
DR Pfam; PF01527; Transposase_8; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 172 AA; 20622 MW; 5187DC04B8407F52 CRC64;

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Query Match 14.4%; Score 85; DB 2; Length 172;
Best Local Similarity 36.8%; Pred. No. 3.1;
Matches 14; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 27 RREYVDLKKRRGRDPENWGKRRKPPQEGLYNELOKD 64
DB 100 KKNRYTVYKTRGRPPKGRKPKKSEMTLELOKKE 137

RESULT 13
Q754G7 PRELIMINARY; PRT; 744 AA.
AC Q754G7;
DT 05-JUL-2004 (TRENDELrel. 27, Created)
DT 05-JUL-2004 (TRENDELrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENDELrel. 27, Last annotation update)
DE AFR103WP.
GN Name=AFR103W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCB1_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX Pubmed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegel S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomycetes cerevisiae genome."
RL Science 304:304-307 (2004).
DR EMBL; AE016901; AAS53474.1; -.
DR AGD; AFR103W; -.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR000261; EFS15_Homology.
DR SMART; SM00027; EH; 1.
DR PROSITE; PS50031; EH; 1.
SQ SEQUENCE 744 AA; 82630 MW; 7DBE05484729D7D1 CRC64;

Query Match 13.8%; Score 81.5; DB 2; Length 744;

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Best Local Similarity 29.3%; Pred. No. 38;
Matches 29; Conservative 17; Mismatches 38; Indels 15; Gaps 5;

QY 4 SSSSEP-----HQLSDS-SESEEDYSDNRSSRSRSGKREKIRNLYRNSF 578
DB 527 SSSSEP-----HQLSDS-SESEEDYSDNRSSRSRSGKREKIRNLYRNSF 578

QY 62 OKDKMAEAYSEIGMKERRRGKHDGLYQGLSTATDITY 100
DB 579 NEDKPMKSHLDVGYTERERKR-----YEGMWVSNNDTY 612

RESULT 14
Q7XK73 PRELIMINARY; PRT; 1123 AA.
AC Q7XK73;
DT 01-OCT-2003 (TRENBLREL. 25, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DE OSJNBao028M15.14 protein.
GN Name=OSJNBao028M15.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_Taxid=39947;
[1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Lu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Wang Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian X.W., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Mu M., Zhang R.Q., Guan J.P., Gu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL662961; CAB05822.1; -
DR Gramene; Q7XK73; -
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR005162; Retrotrans_gag
DR InterPro; IPR008916; Retrov_capsid_C.
DR pfam; PF003732; Retrotrans_gag; 1.
DR pfam; PF00078; RVT_1; 1.
KM RNA-directed DNA polymerase; Transferase.
SO SEQUENCE 1123 AA; 125576 MW; 6BBF199DPB92A32 CRC64;

Query Match 13.7%; Score 81; DB 2; Length 1123;
Best Local Similarity 26.6%; Pred. No. 69;
Matches 34; Conservative 13; Mismatches 45; Indels 36; Gaps 6;

QY 5 BSAEPAYQGGONLYNEINLGRREYDVL-----KRGDPEMGKPRKAKQ 54
DB 356 RQATPP--PRGTSIDLHLN-GRRRARRTRDMENRRHVRYSRRHNEGGGLSENQD 412
QY 55 EGLYNELQDKMAEAYSEIGMKERRRG-----KGHDGLYQGLSTATDITY-- 100
DB 413 DNRRNRREHDN-----REQMRGDTTRGCRANDDDGDCRDNGLMQPFVNFQTYKR 467
QY 101 ----DALH 104
DB 468 HTIEDDLH 475

RESULT 15
Q19579 PRELIMINARY; PRT; 692 AA.
AC Q19579;
ID Q19579;
Q19579;

DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Hypothetical protein F18H3.3a.
GN Name=pab-2; Synonyms=F18H3.3a; ORFNames=F18H3.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_Taxid=6239;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=9069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Colas L.;
RT Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50110; CA80444.1; -
DR F1R; T21095; T21095.
DR HSSP; P11940; 1CIVJ.
DR WormBase; WBGene0003903; pab-2.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002004; PAB/HD.
DR InterPro; IPR006515; PAB_1234.
DR InterPro; IPR005054; RNA_rec_mot.
DR pfam; PF00658; PABP; 1.
DR pfam; PF00076; RRM_1; 4.
DR SMART; SM00517; PolyA; 1.
DR SMART; SM00360; RRM; 4.
DR TIGRFAMs; TIGR01628; PABP-1234; 1.
DR PROSITE; PS0102; RRM; 4.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_3.
KM Hypothetical protein.
SO SEQUENCE 692 AA; 75982 MW; D86D7391304AE773 CRC64;

Query Match 13.5%; Score 80; DB 2; Length 692;
Best Local Similarity 21.7%; Pred. No. 48;
Matches 30; Conservative 22; Mismatches 40; Indels 46; Gaps 6;

QY 9 PAYQGGONLYNEINLGRREYDVLDKRRGRDP----- 42
DB 486 PPGQRFQNMFMQYFNFQRYV--PQGGRRPWRKTNDGRDQYGMAPPAGAPVGGPG 542
QY 43 -EMGKPRKKN-----POEGLYNELQDKMAEAYSEIGMKERRRGKHDGL-YQGLS 93
DB 543 VOMGAPLIRQGPAPRAGAPQKPFYQPPRQGPQHSQPPAQPGQGGGSGIVIHGE 602
QY 94 TATKDYDALHM--QALP 109
DB 603 TLTS-----HMLAQAP 614

Search completed: March 7, 2005, 07:19:37
Job time : 45.1298 secs

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